

**Amendments to the claims:**

Please amend the claims as shown below.

- (Currently Amended) A composition comprising a substantially purified AvIII peptide with cellulase activity and, ~~said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74 Ace) enzyme and a carbohydrate binding domain (CBD) III.~~, ~~the catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII\_Ace):~~

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GH74_Ace      AFTQPTTWGVAIGGGG FVDSIVFNGCAPGILYRTDICCNRMBAAACRNIFLLDMWG
AvIII_Ace     AAGQAVTWGIVVTGGCGGFTPGIVFNPBAKVAYARTDICCAYRLNSDD TWTPLHNVWG
*****
GH74_Ace      WNNWGINGVVCIADDPINTNKVWAAVGMVTNSWDPNDCAILRSDQCATWQITPLPKLG
AvIII_Ace     NPIWHDNGIDALATDPVDTRVAVAVGMVTNSWDPNVGGILRSTDCGPTWFTTKLPKVG
*****
GH74_Ace      CNMPCRCMGERLAVDPNEDNELYFCAPGCKGLWRSTDGCAWQGMNTTFDVCTVIANDTD
AvIII_Ace     CNMPCRCMGERLAVDPNNGTILYFCARGCHGLWRSTDYCATWNSVTSFTWCTCTYQDSGS
*****
GH74_Ace      TPGVSSDIQCIAWAADFKAESSLCQAKETIFGVADPNNPVFWCRDCCATWQAVPGAP T
AvIII_Ace     T YTSDFVGIAMVTFBETGCGCGCATTRIFGVADAGKGVTKGEBAGATWVAUSCEPQV
*****
GH74_Ace      GPFPKGVTFDPVNHVLYIATGNTGCPYDCSSCDVHKFSUTSCTWTRISDPVSTDIANDYP
AvIII_Ace     GFLPHKCVLSPEKTLVIGYANGACPYDGTNGTAKVNTSGVWTDIST TGLASTFY
*****
GH74_Ace      CYGCLTIDRQHPTTIVATQICSWPDTIIFRSTDCGATNRIWDWISVNRSLAYVLDIS
AvIII_Ace     GVGGLVDLQVDCTLMVAALNCNWDELIFRSTDCATNGPIWENNGYPCINVYVSYDGS
*****
GH74_Ace      AEFWLTPGVQPNDFVPGPKLNMDEAMAIDPFNSDRMLYCTGATLYATNBLTKWDSGCGI
AvIII_Ace     NADWIGDTTSTDQFE VRVGMVVEALAIIDPFDSNHLYCTGLTVGGHDLTNWDSKHPV
*****
GH74_Ace      HIRPWKGLSETAVNDLICFPFGCAPLICALCDLCCETHADVTAVDPSTIFTSPVETCTSV
AvIII_Ace     TVKCLAVGIEEMAVLGLITFPGCPALLSAVCDDCGFYHSDLDAAAPQAVHTPTVCTNGI
*****
GH74_Ace      DYAEINPGLIIVRAGSFDPSGQNDNVAFSTDCGHWPFQCGEPGGVTFGCTVAASADGR
AvIII_Ace     DYACNKPENIVRSGAGDYP TLALCGNPGCTWFDYAACTGTCTCAVALSADGDT
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GH74_Aac ----- FVWAPEDDCQPIVAVGFCNENWALSCGVFANAQIRSDRVNDKTFYALCNGTFYRSTDDGV
AviIII_Aac ----- VLLMSSTGCAVSKKCGC TLTAVSSLDGCAVIASDKSDNTFVYGGGACAIYVSIQTAT
-----
GH74_Aac ----- TFQPVIAGLPSSCAVGVMTHTAVTCKEEDLWLAACSELVHSTNCGGSGWCAI TCVSSAVNV
AviIII_Aac ----- SFTKTVG LGGSTTVNAIR AHPGIAEDWVACTDKOLWISTDYCSTFTQICGCVTAGNCF
-----
GH74_Aac ----- CPCKSADGSCYPAVFVGTIGGVTCAYRSDDECTTFWLINDDQHGVEN WQATTCDHAN
AviIII_Aac ----- CPCKASCTGGVTVVYCGFTTIDCAAGLFRKSDAGTNWQVIGDASNGPSSCSANFANGDLQT
-----
GH74_Aac ----- LRRVVECTNRCGIVVGBICGAPCG
AviIII_Aac ----- YCRVFRCHERRPCHLLNQCQRBPAG
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2. (Previously Presented) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.
3. (Cancelled)
4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.
8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
9. (Previously Presented) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74\_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated AvIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvIII polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

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GH74_Ace      ATTQPYTNSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRMDAANGRWIPLLDVWG
AviIII_Aac    AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPIMDVWG
               *::*,**,**, **** , ***** , * : *,***** ** :: : * **;***

GH74_Ace      WNWGYNGVVSIAADPINTNKVMAAVGMYTNSMDPNDGAILRSSDQGATWQITPLPFFKL
AviIII_Aac    NDTWHDNGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDWTWTETKLPFKV
               :,* ** : :*,*:**::*,*:*****,* ** *;****,* **;***

GH74_Ace      GNMFGRGNGERLAVDPNNNDILYFGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD
AviIII_Aac    GNMFGRGNGERLAVDPNKNLSILYFGARSGHGLWKSTDYGAATSNVTSFTWTGTGYQDSSS
               *****G*****::,* **** **;***,* ** *****:*,* . **; :..

GH74_Ace      TCGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac    T--YTSDFVGIAVNTFDSTSGSGSATPRI FVGVADAGKSVFKSEDAGATWAVWSGEPQY
               * * ** * :*,**;*,*:*,* *,* : ***** :..* * * *,* ** ** *

GH74_Ace      GPPIPHKGVFDPVNHVLIATISNTGCPYDGGSSGDVWKFBSVTSGTWTRISFPVSTDTANDYF
AviIII_Aac    GFLPHKGVLSPPEKTLTYSYANGAGPYDGTNGTVHKYNI TSGVWTDISP---TSLASTYY
               * * * * * : * * * * * : * * * * * * * : * * * * * * * : * * * * *

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PAGE 11/13 \* RCVD AT 9/29/2005 3:24:39 PM [Eastern Daylight Time] \* SVR:USPTO-EFXRF-6/25 \* DNIS:2738300 \* CSID:7209313001 \* DURATION (mm-ss):02-48

54. (New) The composition of claim 51 wherein said catalytic domain GH74\_Ace has a sequence identical to SEQ ID NO. 3.